

SEQUENCE LISTING

<110> Barbet, Anthony F.
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<120> Nucleic Acid Vaccines Against Rickettsial Diseases and
 Methods of use

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 <151> 2000-04-21

<150> 09/337,827
 <151> 1999-06-22

<150> 08/953,326
 <151> 1997-10-17

<150> 08/733,230
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<150> 60/130,725
 <151> 1999-04-22

<150> 60/269,944
 <151> 2001-02-20

<160> 34

<170> PatentIn Ver. 2.0

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Asn Pro Ala Gly Ser Val Tyr Ile Ser Ala Lys Tyr Met Pro Thr Ala	
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tca cat ttt ggt aaa atg tca atc aaa gaa gat tca aaa aat act caa	192
Ser His Phe Gly Lys Met Ser Ile Lys Glu Asp Ser Lys Asn Thr Gln	
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acg gta ttt ggt cta aaa aaa gat tgg gat ggc gtt aaa aca cca tca	240
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gat tct agc aat act aat tct aca att ttt act gaa aaa gac tat tct	288
Asp Ser Ser Asn Thr Asn Ser Thr Ile Phe Thr Glu Lys Asp Tyr Ser	
85 90 95	
ttc aga tat gaa aac aat ccg ttt tta ggt ttc gct gga gca att ggg	336
Phe Arg Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly	
100 105 110	
tac tca atg aat gga cca aga ata gag ttc gaa gta tcc tat gaa act	384
Tyr Ser Met Asn Gly Pro Arg Ile Glu Phe Glu Val Ser Tyr Glu Thr	
115 120 125	
ttt gat gta aaa aac cta ggt ggc aac tat aaa aac aac gca cac atg	432
Phe Asp Val Lys Asn Leu Gly Gly Asn Tyr Lys Asn Asn Ala His Met	
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tac tgt gct tta gat aca gca gca caa aat agc act aat ggc gca gga	480
Tyr Cys Ala Leu Asp Thr Ala Ala Gln Asn Ser Thr Asn Gly Ala Gly	
145 150 155 160	
tta act aca tct gtt atg gta aaa aac gaa aat tta aca aat ata tca	528
Leu Thr Thr Ser Val Met Val Lys Asn Glu Asn Leu Thr Asn Ile Ser	
165 170 175	
tta atg tta aat gcg tgt tat gat atc atg ctt gat gga ata cca gtt	576
Leu Met Leu Asn Ala Cys Tyr Asp Ile Met Leu Asp Gly Ile Pro Val	
180 185 190	
tct cca tat gta tgt gca ggt att ggc act gac tta gtg tca gta att	624
Ser Pro Tyr Val Cys Ala Gly Ile Gly Thr Asp Leu Val Ser Val Ile	
195 200 205	
aat gct aca aat cct aaa tta tct tat caa gga aag cta ggc ata agt	672
Asn Ala Thr Asn Pro Lys Leu Ser Tyr Gln Gly Lys Leu Gly Ile Ser	
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225 230 235 240	

aga gtt ata ggt aat gaa ttt aaa gat att gct acc tta aaa ata ttt 768
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Ser His Phe Gly Lys Met Ser Ile Lys Glu Asp Ser Lys Asn Thr Gln
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Thr Val Phe Gly Leu Lys Lys Asp Trp Asp Gly Val Lys Thr Pro Ser
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Leu Met Leu Asn Ala Cys Tyr Asp Ile Met Leu Asp Gly Ile Pro Val
 180 185 190

Ser Pro Tyr Val Cys Ala Gly Ile Gly Thr Asp Leu Val Ser Val Ile
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Asn Ala Thr Asn Pro Lys Leu Ser Tyr Gln Gly Lys Leu Gly Ile Ser
 210 215 220

Tyr Ser Ile Asn Ser Glu Ala Ser Ile Phe Ile Gly Gly His Phe His
 225 230 235 240

Arg Val Ile Gly Asn Glu Phe Lys Asp Ile Ala Thr Leu Lys Ile Phe
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Thr Ser Lys Thr Gly Ile Ser Asn Pro Gly Phe Ala Ser Ala Thr Leu
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att aac ggt aat ttc tac atc agt gga aaa tac gat gcc aag gct tcg 144
 Ile Asn Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Asp Ala Lys Ala Ser
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 His Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Thr Thr Val Gly
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 65 70 75 80

tcc cca aac gat gta ttc act gtc tca aat tat tca ttt aaa tat gaa 288
 Ser Pro Asn Asp Val Phe Thr Val Ser Asn Tyr Ser Phe Lys Tyr Glu
 85 90 95

aac aac ccg ttt tta ggt ttt gca gga gct att ggt tac tca atg gat 336
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      145                      150                      155                      160

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tgc tat gac gta gta ggc gaa ggc ata cct ttt tct cct tat ata tgc 576
Cys Tyr Asp Val Val Gly Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys
      180                      185                      190

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Ala Gly Ile Gly Thr Asp Leu Val Ser Met Phe Glu Ala Thr Asn Pro
      195                      200                      205

aaa att tct tac caa gga aag tta ggt tta agc tac tct ata agc cca 672
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gaa ttt aga gat att cct act ata ata cct act gga tca aca ctt gca 768
Glu Phe Arg Asp Ile Pro Thr Ile Ile Pro Thr Gly Ser Thr Leu Ala
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gga aaa gga aac tac cct gca ata gta ata ctg gat gta tgc cac ttt 816
Gly Lys Gly Asn Tyr Pro Ala Ile Val Ile Leu Asp Val Cys His Phe
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Ser Pro Asn Asp Val Phe Thr Val Ser Asn Tyr Ser Phe Lys Tyr Glu
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Gly Pro Arg Ile Glu Leu Glu Val Ser Tyr Glu Thr Phe Asp Val Lys
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Phe Leu Lys Asn Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala
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Ala Gly Ile Gly Thr Asp Leu Val Ser Met Phe Glu Ala Thr Asn Pro
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Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Ser Pro
      210             215             220
Glu Ala Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn
      225             230             235             240
Glu Phe Arg Asp Ile Pro Thr Ile Ile Pro Thr Gly Ser Thr Leu Ala
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Gly Ile Glu Met Gly Gly Arg Phe
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agt cac gaa gtg gct tct gaa ggg gga gta atg gga ggt agc ttt tac	144
Ser His Glu Val Ala Ser Glu Gly Gly Val Met Gly Gly Ser Phe Tyr	
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agc att gca acg att gat gtg agt gtg cca gca aac ttt tcc aaa tct	288
Ser Ile Ala Thr Ile Asp Val Ser Val Pro Ala Asn Phe Ser Lys Ser	
85 90 95	
ggc tac act ttt gcc ttc tct aaa aac tta atc acg tct ttc gac ggc	336
Gly Tyr Thr Phe Ala Phe Ser Lys Asn Leu Ile Thr Ser Phe Asp Gly	
100 105 110	
gct gtg gga tat tct ctg gga gga gcc aga gtg gaa ttg gaa gcg agc	384
Ala Val Gly Tyr Ser Leu Gly Gly Ala Arg Val Glu Leu Glu Ala Ser	
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tac aga agg ttt gct act ttg gcg gac ggg cag tac gca aaa agt ggt	432
Tyr Arg Arg Phe Ala Thr Leu Ala Asp Gly Gln Tyr Ala Lys Ser Gly	
130 135 140	
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Ala Glu Ser Leu Ala Ala Ile Thr Arg Asp Ala Asn Ile Thr Glu Thr	
145 150 155 160	
aat tac ttc gta gtc aaa att gat gaa atc aca aac acc tca gtc atg	528
Asn Tyr Phe Val Val Lys Ile Asp Glu Ile Thr Asn Thr Ser Val Met	
165 170 175	
tta aat ggc tgc tat gac gtg ctg cac aca gat tta cct gtg tcc ccg	576
Leu Asn Gly Cys Tyr Asp Val Leu His Thr Asp Leu Pro Val Ser Pro	
180 185 190	
tat gta tgt gcc ggg ata ggc gca agc ttt gtt gac atc tct aag caa	624
Tyr Val Cys Ala Gly Ile Gly Ala Ser Phe Val Asp Ile Ser Lys Gln	
195 200 205	

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    225                230                235                240

ttt gat gag tct tac aag gac att ccc gca cac aac agt gta aag ttc 768
Phe Asp Glu Ser Tyr Lys Asp Ile Pro Ala His Asn Ser Val Lys Phe
    245                250                255

tct gga gaa gca aaa gcc tca gtc aaa gcg cat att gct gac tac ggc 816
Ser Gly Glu Ala Lys Ala Ser Val Lys Ala His Ile Ala Asp Tyr Gly
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Val Gly Ala Ala Tyr Ser Pro Ala Phe Pro Ser Val Thr Ser Phe Asp
    50                55                60

Met Arg Glu Ser Ser Lys Glu Thr Ser Tyr Val Arg Gly Tyr Asp Lys
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Ser Ile Ala Thr Ile Asp Val Ser Val Pro Ala Asn Phe Ser Lys Ser
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Gly Tyr Thr Phe Ala Phe Ser Lys Asn Leu Ile Thr Ser Phe Asp Gly
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Ala Val Gly Tyr Ser Leu Gly Gly Ala Arg Val Glu Leu Glu Ala Ser
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Ala Glu Ser Leu Ala Ala Ile Thr Arg Asp Ala Asn Ile Thr Glu Thr

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	180	185	190
Tyr Val Cys Ala Gly Ile Gly Ala Ser Phe Val Asp Ile Ser Lys Gln			
	195	200	205
Val Thr Thr Lys Leu Ala Tyr Arg Gly Lys Val Gly Ile Ser Tyr Gln			
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Phe Thr Pro Glu Ile Ser Leu Val Ala Gly Gly Phe Tyr His Gly Leu			
	225	230	235
Phe Asp Glu Ser Tyr Lys Asp Ile Pro Ala His Asn Ser Val Lys Phe			
	245	250	255
Ser Gly Glu Ala Lys Ala Ser Val Lys Ala His Ile Ala Asp Tyr Gly			
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Phe Asn Leu Gly Ala Arg Phe Leu Phe Ser			
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 ttagggacat tcctactctg aaagcatttg ttacgtcatc agctactcca gatctagcaa 780
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 caggatttgg tactgatctc atatctatgt ttgagacaac acaaaacaaa atatcttatc 660
 aaggaaagtt aggtttaaac tatactataa actcaagagt ttctgttttt gcagggtgggc 720
 actttcataa ggtaatagggt aatgaattta aaggatttcc tactctatta cctgatggat 780
 caaacattaa agtacaacag tctgcaacag taacattaga tgtgtgccat ttcggggttag 840
 agattggaag tagatttttc tttt 864

<210> 13

<211> 399

<212> DNA

<213> Ehrlichia canis

<400> 13

atatgaattg taaaaaagtt ttcacaataa gtgcattgat atcatccata tacttcctac 60
 ctaatgtctc atactctaac ccagtatatg gtaacagtat gtatggtaat ttttacatat 120
 caggaaagta catgccaaagt gttcctcatt ttggaatttt ttcagctgaa gaagagaaaa 180
 aaaagacaac tgtagtatat ggcttaaaag aaaactgggc aggagatgca atatctagtc 240
 aaagtccaga tgataatttt accattcgaa attactcatt caagtatgca agcaacaagt 300
 ttttaggggtt tgcagtagct attgggttact cgataggcag tccaagaata gaagttgaga 360
 tgtcttatga agcatttgat gtaaaaaatc aaggttaaca 399

<210> 14

<211> 43

<212> PRT

<213> Ehrlichia chaffeensis

<400> 14

Asn	Glu	Phe	Arg	Asp	Ile	Ser	Thr	Leu	Lys	Ala	Phe	Ala	Thr	Pro	Ser
1				5					10					15	
Ser	Ala	Ala	Thr	Pro	Asp	Leu	Ala	Thr	Val	Thr	Leu	Ser	Val	Cys	His
			20					25					30		
Phe	Gly	Val	Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe					
		35					40								

<210> 15

<211> 286

<212> PRT

<213> Ehrlichia chaffeensis

<400> 15

Met	Asn	Cys	Glu	Lys	Phe	Phe	Ile	Thr	Thr	Ala	Leu	Thr	Leu	Leu	Met
1				5					10					15	
Ser	Phe	Leu	Pro	Gly	Ile	Ser	Leu	Ser	Asp	Pro	Val	Gln	Asp	Asp	Asn
			20					25					30		
Ile	Ser	Gly	Asn	Phe	Tyr	Ile	Ser	Gly	Lys	Tyr	Met	Pro	Ser	Ala	Ser
		35					40					45			
His	Phe	Gly	Val	Phe	Ser	Ala	Lys	Glu	Glu	Arg	Asn	Thr	Thr	Val	Gly
	50					55					60				
Val	Phe	Gly	Ile	Glu	Gln	Asp	Trp	Asp	Arg	Cys	Val	Ile	Ser	Arg	Thr
65					70				75					80	
Thr	Leu	Ser	Asp	Ile	Phe	Thr	Val	Pro	Asn	Tyr	Ser	Phe	Lys	Tyr	Glu

85					90					95					
Asn	Asn	Leu	Phe	Ser	Gly	Phe	Ala	Gly	Ala	Ile	Gly	Tyr	Ser	Met	Asp
		100						105					110		
Gly	Pro	Arg	Ile	Glu	Leu	Glu	Val	Ser	Tyr	Glu	Ala	Phe	Asp	Val	Lys
		115					120					125			
Asn	Gln	Gly	Asn	Asn	Tyr	Lys	Asn	Glu	Ala	His	Arg	Tyr	Tyr	Ala	Leu
	130					135					140				
Ser	His	Leu	Leu	Gly	Thr	Glu	Thr	Gln	Ile	Asp	Gly	Ala	Gly	Ser	Ala
145					150					155					160
Ser	Val	Phe	Leu	Ile	Asn	Glu	Gly	Leu	Leu	Asp	Lys	Ser	Phe	Met	Leu
			165						170					175	
Asn	Ala	Cys	Tyr	Asp	Val	Ile	Ser	Glu	Gly	Ile	Pro	Phe	Ser	Pro	Tyr
			180						185				190		
Ile	Cys	Ala	Gly	Ile	Gly	Ile	Asp	Leu	Val	Ser	Met	Phe	Glu	Ala	Ile
	195						200					205			
Asn	Pro	Lys	Ile	Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Pro	Ile
	210					215					220				
Ser	Pro	Glu	Ala	Ser	Val	Phe	Ile	Gly	Gly	His	Phe	His	Lys	Val	Ile
225					230					235					240
Gly	Asn	Glu	Phe	Arg	Asp	Ile	Pro	Thr	Met	Ile	Pro	Ser	Glu	Ser	Ala
			245						250					255	
Leu	Ala	Gly	Lys	Gly	Asn	Tyr	Pro	Ala	Ile	Val	Thr	Leu	Asp	Val	Phe
		260						265					270		
Tyr	Phe	Gly	Ile	Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe	Gln	Leu		
		275					280					285			

<210> 16

<211> 278

<212> PRT

<213> Ehrlichia chaffeensis

<400> 16

Met	Asn	Cys	Lys	Lys	Phe	Phe	Ile	Thr	Thr	Ala	Leu	Val	Ser	Leu	Met
1				5					10					15	

Ser	Phe	Leu	Pro	Gly	Ile	Ser	Phe	Ser	Asp	Pro	Val	Gln	Gly	Asp	Asn
		20						25					30		

Ile	Ser	Gly	Asn	Phe	Tyr	Val	Ser	Gly	Lys	Tyr	Met	Pro	Ser	Ala	Ser
		35						40					45		

His	Phe	Gly	Met	Phe	Ser	Ala	Lys	Glu	Glu	Lys	Asn	Pro	Thr	Val	Ala
		50				55					60				

Leu Tyr Gly Leu Lys Gln Asp Trp Glu Gly Ile Ser Ser Ser Ser His
 65 70 75 80
 Asn Asp Asn His Phe Asn Asn Lys Gly Tyr Ser Phe Lys Tyr Glu Asn
 85 90 95
 Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly
 100 105 110
 Pro Arg Val Glu Phe Glu Val Ser Tyr Glu Thr Phe Asp Val Lys Asn
 115 120 125
 Gln Gly Asn Asn Tyr Lys Asn Asp Ala His Arg Tyr Cys Ala Leu Gly
 130 135 140
 Gln Gln Asp Asn Ser Gly Ile Pro Lys Thr Ser Lys Tyr Val Leu Leu
 145 150 155 160
 Lys Ser Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala Cys Tyr
 165 170 175
 Asp Ile Ile Asn Glu Ser Ile Pro Leu Ser Pro Tyr Ile Cys Ala Gly
 180 185 190
 Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Thr Asn Pro Lys Ile
 195 200 205
 Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala
 210 215 220
 Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu Phe
 225 230 235 240
 Arg Asp Ile Pro Thr Leu Lys Ala Phe Val Thr Ser Ser Ala Thr Pro
 245 250 255
 Asp Leu Ala Ile Val Thr Leu Ser Val Cys His Phe Gly Ile Glu Leu
 260 265 270
 Gly Gly Arg Phe Asn Phe
 275

<210> 17

<211> 280

<212> PRT

<213> Ehrlichia chaffeensis

<400> 17

Met Asn Cys Lys Lys Phe Phe Ile Thr Thr Thr Leu Val Ser Leu Met
 1 5 10 15

Ser Phe Leu Pro Gly Ile Ser Phe Ser Asp Ala Val Gln Asn Asp Asn
 20 25 30

Val Gly Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Val Pro Ser Val Ser
 35 40 45

His Phe Gly Val Phe Ser Ala Lys Gln Glu Arg Asn Thr Thr Ile Gly
 50 55 60

Val Phe Gly Leu Lys Gln Asp Trp Asp Gly Ser Thr Ile Ser Lys Asn
 65 70 75 80

Ser Pro Glu Asn Thr Phe Asn Val Pro Asn Tyr Ser Phe Lys Tyr Glu
 85 90 95

Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala Val Gly Tyr Leu Met Asn
 100 105 110

Gly Pro Arg Ile Glu Leu Glu Met Ser Tyr Glu Thr Phe Asp Val Lys
 115 120 125

Asn Gln Gly Asn Asn Tyr Lys Asn Asp Ala His Lys Tyr Tyr Ala Leu
 130 135 140

Thr His Asn Ser Gly Gly Lys Leu Ser Asn Ala Gly Asp Lys Phe Val
 145 150 155 160

Phe Leu Lys Asn Glu Gly Leu Leu Asp Ile Ser Leu Met Leu Asn Ala
 165 170 175

Cys Tyr Asp Val Ile Ser Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys
 180 185 190

Ala Gly Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Ile Asn Pro
 195 200 205

Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Ser Pro
 210 215 220

Glu Ala Ser Val Phe Val Gly Gly His Phe His Lys Val Ile Gly Asn
 225 230 235 240

Glu Phe Arg Asp Ile Pro Ala Met Ile Pro Ser Thr Ser Thr Leu Thr
 245 250 255

Gly Asn His Phe Thr Ile Val Thr Leu Ser Val Cys His Phe Gly Val
 260 265 270

Glu Leu Gly Gly Arg Phe Asn Phe
 275 280

<210> 18

<211> 276

<212> PRT

<213> Ehrlichia chaffeensis

<400> 18

Met Asn Tyr Lys Lys Val Phe Ile Thr Ser Ala Leu Ile Ser Leu Ile

1	5	10	15
Ser Ser Leu Pro Gly Val Ser Phe Ser Asp Pro Ala Gly Ser Gly Ile	20	25	30
Asn Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Ala Ser His	35	40	45
Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Thr Thr Val Gly Val	50	55	60
Phe Gly Leu Lys Gln Asn Trp Asp Gly Ser Ala Ile Ser Asn Ser Ser	65	70	75
Pro Asn Asp Val Phe Thr Val Ser Asn Tyr Ser Phe Lys Tyr Glu Asn	85	90	95
Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Asp Gly	100	105	110
Pro Arg Ile Glu Leu Glu Val Ser Tyr Glu Thr Phe Asp Val Lys Asn	115	120	125
Gln Gly Asn Asn Tyr Lys Asn Glu Ala His Arg Tyr Cys Ala Leu Ser	130	135	140
His Asn Ser Ala Ala Asp Met Ser Ser Ala Ser Asn Asn Phe Val Phe	145	150	155
Leu Lys Asn Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala Cys	165	170	175
Tyr Asp Val Val Gly Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys Ala	180	185	190
Gly Ile Gly Thr Asp Leu Val Ser Met Phe Glu Ala Thr Asn Pro Lys	195	200	205
Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Ser Pro Glu	210	215	220
Ala Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu	225	230	235
Phe Arg Asp Ile Pro Thr Ile Ile Pro Thr Gly Ser Thr Leu Ala Gly	245	250	255
Lys Gly Asn Tyr Pro Ala Ile Val Ile Leu Asp Val Cys His Phe Gly	260	265	270
Ile Glu Met Gly	275		

<210> 19

<211> 287

<212> PRT

<213> Ehrlichia canis

<400> 19

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Met Lys Tyr Lys Lys Thr Phe Thr Val Thr Ala Leu Val Leu Leu Thr
  1             5             10             15

Ser Phe Thr His Phe Ile Pro Phe Tyr Ser Pro Ala Arg Ala Ser Thr
          20             25             30

Ile His Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Thr Ala Ser His
          35             40             45

Phe Gly Ile Phe Ser Ala Lys Glu Glu Gln Ser Phe Thr Lys Val Leu
          50             55             60

Val Gly Leu Asp Gln Arg Leu Ser His Asn Ile Ile Asn Asn Asn Asp
          65             70             75             80

Thr Ala Lys Ser Leu Lys Val Gln Asn Tyr Ser Phe Lys Tyr Lys Asn
          85             90             95

Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Ile Gly Asn
          100            105            110

Ser Arg Ile Glu Leu Glu Val Ser His Glu Ile Phe Asp Thr Lys Asn
          115            120            125

Pro Gly Asn Asn Tyr Leu Asn Asp Ser His Lys Tyr Cys Ala Leu Ser
          130            135            140

His Gly Ser His Ile Cys Ser Asp Gly Asn Ser Gly Asp Trp Tyr Thr
          145            150            155            160

Ala Lys Thr Asp Lys Phe Val Leu Leu Lys Asn Glu Gly Leu Leu Asp
          165            170            175

Val Ser Phe Met Leu Asn Ala Cys Tyr Asp Ile Thr Thr Glu Lys Met
          180            185            190

Pro Phe Ser Pro Tyr Ile Cys Ala Gly Ile Gly Thr Asp Leu Ile Ser
          195            200            205

Met Phe Glu Thr Thr Gln Asn Lys Ile Ser Tyr Gln Gly Lys Leu Gly
          210            215            220

Leu Asn Tyr Thr Ile Asn Ser Arg Val Ser Val Phe Ala Gly Gly His
          225            230            235            240

Phe His Lys Val Ile Gly Asn Glu Phe Lys Gly Ile Pro Thr Leu Leu
          245            250            255

Pro Asp Gly Ser Asn Ile Lys Val Gln Gln Ser Ala Thr Val Thr Leu
          260            265            270

Asp Val Cys His Phe Gly Leu Glu Ile Gly Ser Arg Phe Phe Phe

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275

280

285

<210> 20
 <211> 133
 <212> PRT
 <213> Ehrlichia canis

<400> 20
 Met Asn Cys Lys Lys Val Phe Thr Ile Ser Ala Leu Ile Ser Ser Ile
 1 5 10 15
 Tyr Phe Leu Pro Asn Val Ser Tyr Ser Asn Pro Val Tyr Gly Asn Ser
 20 25 30
 Met Tyr Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Val Pro
 35 40 45
 His Phe Gly Ile Phe Ser Ala Glu Glu Glu Lys Lys Lys Thr Thr Val
 50 55 60
 Val Tyr Gly Leu Lys Glu Asn Trp Ala Gly Asp Ala Ile Ser Ser Gln
 65 70 75 80
 Ser Pro Asp Asp Asn Phe Thr Ile Arg Asn Tyr Ser Phe Lys Tyr Ala
 85 90 95
 Ser Asn Lys Phe Leu Gly Phe Ala Val Ala Ile Gly Tyr Ser Ile Gly
 100 105 110
 Ser Pro Arg Ile Glu Val Glu Met Ser Tyr Glu Ala Phe Asp Val Lys
 115 120 125
 Asn Gln Gly Asn Asn
 130

<210> 21
 <211> 686
 <212> DNA
 <213> Ehrlichia canis

<400> 21
 atgaaagcta tcaaattcat acttaatgtc tgcttactat ttgcagcaat attttttaggg 60
 tattcctata ttacaaaaca aggcataattt caaacaaaac atcatgatac acctaatact 120
 actataccaa atgaagacgg tattcaatct agcttttagct taatcaatca agacggtaaa 180
 acagtaacca gccaaagattt cctagggaaa cacatgttag ttttgtttgg attctctgca 240
 tgtaaaagca ttgcccctgc agaattggga ttagtatctg aagcacttgc acaacttggg 300
 aataatgcag acaaattaca agtaattttt attacaattg atccaaaaaa tgatactgta 360
 gaaaaattaa aagaatttca tgaacatttt gattcaagaa ttcaaattgtt aacaggaaat 420

actgaagaca ttaatcaaat aattaaaaat tataaaatat atgttggaca agcagataaa 480
gatcatcaaa ttaaccattc tgcaataatg taccttattg aaaaaaagg atcatatctt 540
tcacacttca ttccagattt aaaatcacaa gaaaatcaag tagataagtt actatcttta 600
gttaagcagt atctgtaaat aaattcatgg aatacgttgg atgagtaggt tttttttagt 660
atttttagtg ctaataacat tggcat 686

<210> 22
<211> 618
<212> DNA
<213> Ehrlichia chaffeensis

<400> 22
atgaaagtta tcaaatttat acttaatatc tgtttattat ttgcagcaat ttttctagga 60
tattcctacg taacaaaaca aggcattttt caagtaagag atcataacac tccaatata 120
aatatatcaa ataaagccag cattactact agtttttcgt tagtaaataca agatggaaat 180
acagtaaata gtcaagattt tttgggaaaa tacatgctag ttttatttgg attttcttca 240
tgtaaaagca tctgccctgc tgaattagga atagcatctg aagttctctc acagcttggt 300
aatgacacag acaagttaca agtaattttc attacaattg atccaacaaa tgatactgta 360
caaaaattaa aaacatttca tgaacatttt gatcctagaa ttcaaagct aacaggcagt 420
gcagaagata ttgaaaaaat aataaaaaat tacaaaatat atgttggaca agcagataaa 480
gataatcaaa ttgatcactc tgccataatg tacattatcg ataaaaagg agaatacatt 540
tcacactttt ctccagattt aaaatcaaca gaaaatcaag tagataagtt actatctata 600
ataaaacaat atctctaa 618

<210> 23
<211> 205
<212> PRT
<213> Ehrlichia canis

<400> 23
Met Lys Ala Ile Lys Phe Ile Leu Asn Val Cys Leu Leu Phe Ala Ala
1 5 10 15
Ile Phe Leu Gly Tyr Ser Tyr Ile Thr Lys Gln Gly Ile Phe Gln Thr
20 25 30
Lys His His Asp Thr Pro Asn Thr Thr Ile Pro Asn Glu Asp Gly Ile
35 40 45

Gln Ser Ser Phe Ser Leu Ile Asn Gln Asp Gly Lys Thr Val Thr Ser
 50 55 60
 Gln Asp Phe Leu Gly Lys His Met Leu Val Leu Phe Gly Phe Ser Ala
 65 70 75 80
 Cys Lys Ser Ile Cys Pro Ala Glu Leu Gly Leu Val Ser Glu Ala Leu
 85 90 95
 Ala Gln Leu Gly Asn Asn Ala Asp Lys Leu Gln Val Ile Phe Ile Thr
 100 105 110
 Ile Asp Pro Lys Asn Asp Thr Val Glu Lys Leu Lys Glu Phe His Glu
 115 120 125
 His Phe Asp Ser Arg Ile Gln Met Leu Thr Gly Asn Thr Glu Asp Ile
 130 135 140
 Asn Gln Ile Ile Lys Asn Tyr Lys Ile Tyr Val Gly Gln Ala Asp Lys
 145 150 155 160
 Asp His Gln Ile Asn His Ser Ala Ile Met Tyr Leu Ile Asp Lys Lys
 165 170 175
 Gly Ser Tyr Leu Ser His Phe Ile Pro Asp Leu Lys Ser Gln Glu Asn
 180 185 190
 Gln Val Asp Lys Leu Leu Ser Leu Val Lys Gln Tyr Leu
 195 200 205

<210> 24

<211> 205

<212> PRT

<213> Ehrlichia chaffeensis

<400> 24

Met Lys Val Ile Lys Phe Ile Leu Asn Ile Cys Leu Leu Phe Ala Ala
 1 5 10 15
 Ile Phe Leu Gly Tyr Ser Tyr Val Thr Lys Gln Gly Ile Phe Gln Val
 20 25 30
 Arg Asp His Asn Thr Pro Asn Thr Asn Ile Ser Asn Lys Ala Ser Ile
 35 40 45
 Thr Thr Ser Phe Ser Leu Val Asn Gln Asp Gly Asn Thr Val Asn Ser
 50 55 60
 Gln Asp Phe Leu Gly Lys Tyr Met Leu Val Leu Phe Gly Phe Ser Ser
 65 70 75 80
 Cys Lys Ser Ile Cys Pro Ala Glu Leu Gly Ile Ala Ser Glu Val Leu
 85 90 95
 Ser Gln Leu Gly Asn Asp Thr Asp Lys Leu Gln Val Ile Phe Ile Thr

100	105	110
Ile Asp Pro Thr Asn Asp Thr Val Gln Lys Leu Lys Thr Phe His Glu		
115	120	125
His Phe Asp Pro Arg Ile Gln Met Leu Thr Gly Ser Ala Glu Asp Ile		
130	135	140
Glu Lys Ile Ile Lys Asn Tyr Lys Ile Tyr Val Gly Gln Ala Asp Lys		
145	150	155
Asp Asn Gln Ile Asp His Ser Ala Ile Met Tyr Ile Ile Asp Lys Lys		
165	170	175
Gly Glu Tyr Ile Ser His Phe Ser Pro Asp Leu Lys Ser Thr Glu Asn		
180	185	190
Gln Val Asp Lys Leu Leu Ser Ile Ile Lys Gln Tyr Leu		
195	200	205

<210> 25

<211> 618

<212> DNA

<213> Cowdria ruminantium

<220>

<221> CDS

<222> (1)..(615)

<400> 25

atg aag gct atc aag ttt ata ctt aat cta tgt tta cta ttt gca gca	48
Met Lys Ala Ile Lys Phe Ile Leu Asn Leu Cys Leu Leu Phe Ala Ala	
1 5 10 15	
att ttt ttg gga tat tct tac ata aca aaa caa ggt ata ttc caa cca	96
Ile Phe Leu Gly Tyr Ser Tyr Ile Thr Lys Gln Gly Ile Phe Gln Pro	
20 25 30	
aaa tta cac gac tct cct gat gtt aat ata tcg aac aaa gcg gat ata	144
Lys Leu His Asp Ser Pro Asp Val Asn Ile Ser Asn Lys Ala Asp Ile	
35 40 45	
aat act agc ttt agc tta att aat cag gat ggt att acg ata tct agt	192
Asn Thr Ser Phe Ser Leu Ile Asn Gln Asp Gly Ile Thr Ile Ser Ser	
50 55 60	
aaa gac ttc ctt gga aaa cat atg tta gtc ctt ttt ggg ttt tct tct	240
Lys Asp Phe Leu Gly Lys His Met Leu Val Leu Phe Gly Phe Ser Ser	
65 70 75 80	
tgt aaa act att tgc ccc atg gaa cta ggg tta gca tcc aca att cta	288
Cys Lys Thr Ile Cys Pro Met Glu Leu Gly Leu Ala Ser Thr Ile Leu	
85 90 95	
gat caa ctt ggc aac gaa tct gac aag tta caa gta gtc ttt ata act	336

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Asp Gln Leu Gly Asn Glu Ser Asp Lys Leu Gln Val Val Phe Ile Thr
      100                      105                      110

att gat cca aca aaa gat act gta gaa aca cta aaa gag ttt cac aaa 384
Ile Asp Pro Thr Lys Asp Thr Val Glu Thr Leu Lys Glu Phe His Lys
      115                      120                      125

aat ttt gac tca cgg att caa atg tta aca gga aac att gaa gct att 432
Asn Phe Asp Ser Arg Ile Gln Met Leu Thr Gly Asn Ile Glu Ala Ile
      130                      135                      140

aat caa ata gta caa ggg tac aaa gta tat gta ggt cag cca gac aat 480
Asn Gln Ile Val Gln Gly Tyr Lys Val Tyr Val Gly Gln Pro Asp Asn
      145                      150                      155                      160

gat aac caa att aac cat tct gga ata atg tat att gta gac aag aaa 528
Asp Asn Gln Ile Asn His Ser Gly Ile Met Tyr Ile Val Asp Lys Lys
      165                      170                      175

gga gaa tat tta aca cat ttt gta cca gat tta aag tca aaa gag cct 576
Gly Glu Tyr Leu Thr His Phe Val Pro Asp Leu Lys Ser Lys Glu Pro
      180                      185                      190

caa gtg gat aaa tta ctt tct tta att aag cag tat ctt taa 618
Gln Val Asp Lys Leu Leu Ser Leu Ile Lys Gln Tyr Leu
      195                      200                      205

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<210> 26

<211> 205

<212> PRT

<213> Cowdria ruminantium

<400> 26

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Met Lys Ala Ile Lys Phe Ile Leu Asn Leu Cys Leu Leu Phe Ala Ala
  1                      5                      10                      15

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Ile Phe Leu Gly Tyr Ser Tyr Ile Thr Lys Gln Gly Ile Phe Gln Pro
      20                      25                      30

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Lys Leu His Asp Ser Pro Asp Val Asn Ile Ser Asn Lys Ala Asp Ile
      35                      40                      45

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Asn Thr Ser Phe Ser Leu Ile Asn Gln Asp Gly Ile Thr Ile Ser Ser
      50                      55                      60

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Lys Asp Phe Leu Gly Lys His Met Leu Val Leu Phe Gly Phe Ser Ser
      65                      70                      75                      80

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Cys Lys Thr Ile Cys Pro Met Glu Leu Gly Leu Ala Ser Thr Ile Leu
      85                      90                      95

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Asp Gln Leu Gly Asn Glu Ser Asp Lys Leu Gln Val Val Phe Ile Thr
      100                      105                      110

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Ile Asp Pro Thr Lys Asp Thr Val Glu Thr Leu Lys Glu Phe His Lys

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115	120	125
Asn Phe Asp Ser Arg Ile Gln Met Leu Thr Gly Asn Ile Glu Ala Ile		
130	135	140
Asn Gln Ile Val Gln Gly Tyr Lys Val Tyr Val Gly Gln Pro Asp Asn		
145	150	155
Asp Asn Gln Ile Asn His Ser Gly Ile Met Tyr Ile Val Asp Lys Lys		
	165	170
Gly Glu Tyr Leu Thr His Phe Val Pro Asp Leu Lys Ser Lys Glu Pro		
	180	185
Gln Val Asp Lys Leu Leu Ser Leu Ile Lys Gln Tyr Leu		
195	200	205

<210> 27

<211> 981

<212> DNA

<213> Cowdria ruminantium

<220>

<221> CDS

<222> (1) .. (978)

<400> 27

atg aag aaa ata ttg gtt acg ttt tta gtt gtt gtt aat gtg ttt tgt	48
Met Lys Lys Ile Leu Val Thr Phe Leu Val Val Val Asn Val Phe Cys	
1 5 10 15	
aat gct gcc att gct tca act gac tca tca gaa gat aaa cag tat att	96
Asn Ala Ala Ile Ala Ser Thr Asp Ser Ser Glu Asp Lys Gln Tyr Ile	
20 25 30	
tta att ggt act ggt tct atg act gga gta tat tat cct ata gga ggt	144
Leu Ile Gly Thr Gly Ser Met Thr Gly Val Tyr Tyr Pro Ile Gly Gly	
35 40 45	
agc ata tgt agg ttt att gca tct gat tat ggt aat gat aat aac agc	192
Ser Ile Cys Arg Phe Ile Ala Ser Asp Tyr Gly Asn Asp Asn Asn Ser	
50 55 60	
ata gtt tgt tct ata tct tct aca act ggt agc gta tat aat ctt aat	240
Ile Val Cys Ser Ile Ser Ser Thr Thr Gly Ser Val Tyr Asn Leu Asn	
65 70 75 80	
tct atg cgt tat gca aat atg gat ata ggt att att caa tct gat tta	288
Ser Met Arg Tyr Ala Asn Met Asp Ile Gly Ile Ile Gln Ser Asp Leu	
85 90 95	
gag tac tat gca tat aat ggt att ggt tta tat gaa aaa atg cca gca	336
Glu Tyr Tyr Ala Tyr Asn Gly Ile Gly Leu Tyr Glu Lys Met Pro Ala	
100 105 110	

atg agg cat cta aga ata tta tct tca tta cat aaa gaa tat ctt aca	384
Met Arg His Leu Arg Ile Leu Ser Ser Leu His Lys Glu Tyr Leu Thr	
115 120 125	
att gtt gtt agg gcg aat tct aat ata tca gtt att gat gat ata aaa	432
Ile Val Val Arg Ala Asn Ser Asn Ile Ser Val Ile Asp Asp Ile Lys	
130 135 140	
ggc aaa aga gtt aat att ggt agt cct ggt act ggt gta aga ata gca	480
Gly Lys Arg Val Asn Ile Gly Ser Pro Gly Thr Gly Val Arg Ile Ala	
145 150 155 160	
atg tta aaa ttg tta aat gaa aaa gga tgg gga aga aaa gat ttt gct	528
Met Leu Lys Leu Leu Asn Glu Lys Gly Trp Gly Arg Lys Asp Phe Ala	
165 170 175	
gtt atg gca gaa tta aaa tca tca gag caa gct caa gca tta tgt gat	576
Val Met Ala Glu Leu Lys Ser Ser Glu Gln Ala Gln Ala Leu Cys Asp	
180 185 190	
aat aaa att gat gtg atg gta gat gtt gtt gga cat cct aat gct gca	624
Asn Lys Ile Asp Val Met Val Asp Val Val Gly His Pro Asn Ala Ala	
195 200 205	
att caa gaa gca gca gca act tgt gat ata aaa ttt att tct tta gat	672
Ile Gln Glu Ala Ala Ala Thr Cys Asp Ile Lys Phe Ile Ser Leu Asp	
210 215 220	
gat gat ctc ata gat aaa tta cat act aag tat ccc tat tat aaa agg	720
Asp Asp Leu Ile Asp Lys Leu His Thr Lys Tyr Pro Tyr Tyr Lys Arg	
225 230 235 240	
gat att att agt ggt gcg tta tac agt aac tta cct gat ata caa act	768
Asp Ile Ile Ser Gly Ala Leu Tyr Ser Asn Leu Pro Asp Ile Gln Thr	
245 250 255	
gtt tca gta aaa gct tct tta ata aca act act gaa tta agc aat gag	816
Val Ser Val Lys Ala Ser Leu Ile Thr Thr Thr Glu Leu Ser Asn Glu	
260 265 270	
ttg gcc tat aaa gtt gtt aaa tct ttg gtt agc cat tta cat gaa cta	864
Leu Ala Tyr Lys Val Val Lys Ser Leu Val Ser His Leu His Glu Leu	
275 280 285	
cat gga att act gga gct ctt aga aat ctt act gta aaa gac atg gta	912
His Gly Ile Thr Gly Ala Leu Arg Asn Leu Thr Val Lys Asp Met Val	
290 295 300	
cag tca gat att aca cct tta cat gac ggt gca aaa cgt tat tat aag	960
Gln Ser Asp Ile Thr Pro Leu His Asp Gly Ala Lys Arg Tyr Tyr Lys	
305 310 315 320	
gaa att gga gtt ata aaa taa	981
Glu Ile Gly Val Ile Lys	
325	

<210> 28
 <211> 326
 <212> PRT
 <213> Cowdria ruminantium

<400> 28

Met	Lys	Lys	Ile	Leu	Val	Thr	Phe	Leu	Val	Val	Val	Asn	Val	Phe	Cys	1	5	10	15
Asn	Ala	Ala	Ile	Ala	Ser	Thr	Asp	Ser	Ser	Glu	Asp	Lys	Gln	Tyr	Ile	20	25	30	
Leu	Ile	Gly	Thr	Gly	Ser	Met	Thr	Gly	Val	Tyr	Tyr	Pro	Ile	Gly	Gly	35	40	45	
Ser	Ile	Cys	Arg	Phe	Ile	Ala	Ser	Asp	Tyr	Gly	Asn	Asp	Asn	Asn	Ser	50	55	60	
Ile	Val	Cys	Ser	Ile	Ser	Ser	Thr	Thr	Gly	Ser	Val	Tyr	Asn	Leu	Asn	65	70	75	80
Ser	Met	Arg	Tyr	Ala	Asn	Met	Asp	Ile	Gly	Ile	Ile	Gln	Ser	Asp	Leu	85	90	95	
Glu	Tyr	Tyr	Ala	Tyr	Asn	Gly	Ile	Gly	Leu	Tyr	Glu	Lys	Met	Pro	Ala	100	105	110	
Met	Arg	His	Leu	Arg	Ile	Leu	Ser	Ser	Leu	His	Lys	Glu	Tyr	Leu	Thr	115	120	125	
Ile	Val	Val	Arg	Ala	Asn	Ser	Asn	Ile	Ser	Val	Ile	Asp	Asp	Ile	Lys	130	135	140	
Gly	Lys	Arg	Val	Asn	Ile	Gly	Ser	Pro	Gly	Thr	Gly	Val	Arg	Ile	Ala	145	150	155	160
Met	Leu	Lys	Leu	Leu	Asn	Glu	Lys	Gly	Trp	Gly	Arg	Lys	Asp	Phe	Ala	165	170	175	
Val	Met	Ala	Glu	Leu	Lys	Ser	Ser	Glu	Gln	Ala	Gln	Ala	Leu	Cys	Asp	180	185	190	
Asn	Lys	Ile	Asp	Val	Met	Val	Asp	Val	Val	Gly	His	Pro	Asn	Ala	Ala	195	200	205	
Ile	Gln	Glu	Ala	Ala	Ala	Thr	Cys	Asp	Ile	Lys	Phe	Ile	Ser	Leu	Asp	210	215	220	
Asp	Asp	Leu	Ile	Asp	Lys	Leu	His	Thr	Lys	Tyr	Pro	Tyr	Tyr	Lys	Arg	225	230	235	240
Asp	Ile	Ile	Ser	Gly	Ala	Leu	Tyr	Ser	Asn	Leu	Pro	Asp	Ile	Gln	Thr	245	250	255	
Val	Ser	Val	Lys	Ala	Ser	Leu	Ile	Thr	Thr	Thr	Glu	Leu	Ser	Asn	Glu				

260	265	270
Leu Ala Tyr Lys Val Val Lys Ser	Leu Val Ser His	Leu His Glu Leu
275	280	285
His Gly Ile Thr Gly Ala Leu Arg Asn	Leu Thr Val Lys Asp Met Val	
290	295	300
Gln Ser Asp Ile Thr Pro Leu His Asp Gly	Ala Lys Arg Tyr Tyr Lys	
305	310	315 320
Glu Ile Gly Val Ile Lys		
325		

<210> 29
 <211> 519
 <212> DNA
 <213> Cowdria ruminantium

<220>
 <221> CDS
 <222> (1)..(516)

<400> 29	
atg aat ata ttc aat tat atg cag ata atg cct aat ata agt gtt gat	48
Met Asn Ile Phe Asn Tyr Met Gln Ile Met Pro Asn Ile Ser Val Asp	
1 5 10 15	
gca ttt gtt gca cct act gct gta att ata ggt gat gtt tgt gta aat	96
Ala Phe Val Ala Pro Thr Ala Val Ile Ile Gly Asp Val Cys Val Asn	
20 25 30	
gac aag tgt agc att tgg tat aac tca gta tta cgt gga gat gta ggc	144
Asp Lys Cys Ser Ile Trp Tyr Asn Ser Val Leu Arg Gly Asp Val Gly	
35 40 45	
caa att gtt att ggt gta ggt act aat att caa gat ggg aca ata ata	192
Gln Ile Val Ile Gly Val Gly Thr Asn Ile Gln Asp Gly Thr Ile Ile	
50 55 60	
cat gtt gat agg aaa tat ggt aat acg aat att ggc aaa aag gtt act	240
His Val Asp Arg Lys Tyr Gly Asn Thr Asn Ile Gly Lys Lys Val Thr	
65 70 75 80	
att ggg cat ggg tgt ata tta cat gct tgt gag ata caa gat tat gtg	288
Ile Gly His Gly Cys Ile Leu His Ala Cys Glu Ile Gln Asp Tyr Val	
85 90 95	
ctt gtt gga atg gga tct att att atg gat aac gtt gtg gtt gaa aag	336
Leu Val Gly Met Gly Ser Ile Ile Met Asp Asn Val Val Val Glu Lys	
100 105 110	
aat gca atg gtg gct gct gga tca tta gtg gta aga ggt aaa gtt gtg	384
Asn Ala Met Val Ala Ala Gly Ser Leu Val Val Arg Gly Lys Val Val	
115 120 125	

aaa act ggt gaa tta tgg gct ggt agg cct gca caa ttt tta aga atg 432
 Lys Thr Gly Glu Leu Trp Ala Gly Arg Pro Ala Gln Phe Leu Arg Met
 130 135 140

ttg tct agt gat gaa att aaa gag ata agt aaa tct gct gat aac tat 480
 Leu Ser Ser Asp Glu Ile Lys Glu Ile Ser Lys Ser Ala Asp Asn Tyr
 145 150 155 160

ata gag ctt gcc agt gat tac ata act ggt aag ttg taa 519
 Ile Glu Leu Ala Ser Asp Tyr Ile Thr Gly Lys Leu
 165 170

<210> 30
 <211> 172
 <212> PRT
 <213> Cowdria ruminantium

<400> 30
 Met Asn Ile Phe Asn Tyr Met Gln Ile Met Pro Asn Ile Ser Val Asp
 1 5 10 15

Ala Phe Val Ala Pro Thr Ala Val Ile Ile Gly Asp Val Cys Val Asn
 20 25 30

Asp Lys Cys Ser Ile Trp Tyr Asn Ser Val Leu Arg Gly Asp Val Gly
 35 40 45

Gln Ile Val Ile Gly Val Gly Thr Asn Ile Gln Asp Gly Thr Ile Ile
 50 55 60

His Val Asp Arg Lys Tyr Gly Asn Thr Asn Ile Gly Lys Lys Val Thr
 65 70 75 80

Ile Gly His Gly Cys Ile Leu His Ala Cys Glu Ile Gln Asp Tyr Val
 85 90 95

Leu Val Gly Met Gly Ser Ile Ile Met Asp Asn Val Val Val Glu Lys
 100 105 110

Asn Ala Met Val Ala Ala Gly Ser Leu Val Val Arg Gly Lys Val Val
 115 120 125

Lys Thr Gly Glu Leu Trp Ala Gly Arg Pro Ala Gln Phe Leu Arg Met
 130 135 140

Leu Ser Ser Asp Glu Ile Lys Glu Ile Ser Lys Ser Ala Asp Asn Tyr
 145 150 155 160

Ile Glu Leu Ala Ser Asp Tyr Ile Thr Gly Lys Leu
 165 170

<210> 31
 <211> 753

<212> DNA

<213> Cowdria ruminantium

<220>

<221> CDS

<222> (1)..(750)

<400> 31

atg atg ata aga atc ttt ctt ttg tta ggc tta gta tta tta gta gca	48
Met Met Ile Arg Ile Phe Leu Leu Leu Gly Leu Val Leu Leu Val Ala	
1 5 10 15	
agt ttt cca cta tta aat aac tgg cta tct aat cat tct ggt aag tct	96
Ser Phe Pro Leu Leu Asn Asn Trp Leu Ser Asn His Ser Gly Lys Ser	
20 25 30	
act aca ttg gat aag gat gca gtt ata tct ata gtt gag gaa tat ata	144
Thr Thr Leu Asp Lys Asp Ala Val Ile Ser Ile Val Glu Glu Tyr Ile	
35 40 45	
acc aat tat cct cag agg gta ata gat tta ctt act aca ggc caa gca	192
Thr Asn Tyr Pro Gln Arg Val Ile Asp Leu Leu Thr Thr Gly Gln Ala	
50 55 60	
caa gca gaa aga gca gag ctt act gaa aat att aaa aaa tat aaa tct	240
Gln Ala Glu Arg Ala Glu Leu Thr Glu Asn Ile Lys Lys Tyr Lys Ser	
65 70 75 80	
gag ctt gaa gat att gca tac cca tct gct ggc aat aaa gac agt aaa	288
Glu Leu Glu Asp Ile Ala Tyr Pro Ser Ala Gly Asn Lys Asp Ser Lys	
85 90 95	
att gca ttt att gag ttc ttc gat tac tct tgt ggt tat tgt aaa atg	336
Ile Ala Phe Ile Glu Phe Phe Asp Tyr Ser Cys Gly Tyr Cys Lys Met	
100 105 110	
atg ttt gaa gat atc aaa caa att ata aaa gat ggt aag gta cgt gtt	384
Met Phe Glu Asp Ile Lys Gln Ile Ile Lys Asp Gly Lys Val Arg Val	
115 120 125	
att ttt aga gat ttt cca ata ctt ggg gaa tcg tcg tta aag gct gtt	432
Ile Phe Arg Asp Phe Pro Ile Leu Gly Glu Ser Ser Leu Lys Ala Val	
130 135 140	
aaa gca gca ttg gct gta cat ctt atc aat cca agt aaa tac ttg gac	480
Lys Ala Ala Leu Ala Val His Leu Ile Asn Pro Ser Lys Tyr Leu Asp	
145 150 155 160	
ttc tat tat gca gca tta aat cat aaa cag cca ttt aat gat gaa tct	528
Phe Tyr Tyr Ala Ala Leu Asn His Lys Gln Pro Phe Asn Asp Glu Ser	
165 170 175	
ata ctt aat ata gtt aaa tca ctt gaa att tca gaa gag gaa ttt aaa	576
Ile Leu Asn Ile Val Lys Ser Leu Glu Ile Ser Glu Glu Glu Phe Lys	
180 185 190	

gat tct tta tct aaa aat tct agt act att gat aag atg ata gag tcc 624
Asp Ser Leu Ser Lys Asn Ser Ser Thr Ile Asp Lys Met Ile Glu Ser
195 200 205

act aga aat ctg gct gag aag tta aat atc aga ggt act cct gct ctt 672
Thr Arg Asn Leu Ala Glu Lys Leu Asn Ile Arg Gly Thr Pro Ala Leu
210 215 220

ata ata ggt gat gca ttc att ggg gga gct gca gat tta tca act tta 720
Ile Ile Gly Asp Ala Phe Ile Gly Gly Ala Ala Asp Leu Ser Thr Leu
225 230 235 240

aga agt aaa ata gta gaa cag cag gaa caa taa 753
Arg Ser Lys Ile Val Glu Gln Gln Glu Gln
245 250

<210> 32
<211> 250
<212> PRT
<213> Cowdria ruminantium

<400> 32
Met Met Ile Arg Ile Phe Leu Leu Leu Gly Leu Val Leu Leu Val Ala
1 5 10 15

Ser Phe Pro Leu Leu Asn Asn Trp Leu Ser Asn His Ser Gly Lys Ser
20 25 30

Thr Thr Leu Asp Lys Asp Ala Val Ile Ser Ile Val Glu Glu Tyr Ile
35 40 45

Thr Asn Tyr Pro Gln Arg Val Ile Asp Leu Leu Thr Thr Gly Gln Ala
50 55 60

Gln Ala Glu Arg Ala Glu Leu Thr Glu Asn Ile Lys Lys Tyr Lys Ser
65 70 75 80

Glu Leu Glu Asp Ile Ala Tyr Pro Ser Ala Gly Asn Lys Asp Ser Lys
85 90 95

Ile Ala Phe Ile Glu Phe Phe Asp Tyr Ser Cys Gly Tyr Cys Lys Met
100 105 110

Met Phe Glu Asp Ile Lys Gln Ile Ile Lys Asp Gly Lys Val Arg Val
115 120 125

Ile Phe Arg Asp Phe Pro Ile Leu Gly Glu Ser Ser Leu Lys Ala Val
130 135 140

Lys Ala Ala Leu Ala Val His Leu Ile Asn Pro Ser Lys Tyr Leu Asp
145 150 155 160

Phe Tyr Tyr Ala Ala Leu Asn His Lys Gln Pro Phe Asn Asp Glu Ser
165 170 175

Ile Leu Asn Ile Val Lys Ser Leu Glu Ile Ser Glu Glu Glu Phe Lys
 180 185 190

Asp Ser Leu Ser Lys Asn Ser Ser Thr Ile Asp Lys Met Ile Glu Ser
 195 200 205

Thr Arg Asn Leu Ala Glu Lys Leu Asn Ile Arg Gly Thr Pro Ala Leu
 210 215 220

Ile Ile Gly Asp Ala Phe Ile Gly Gly Ala Ala Asp Leu Ser Thr Leu
 225 230 235 240

Arg Ser Lys Ile Val Glu Gln Gln Glu Gln
 245 250

<210> 33
 <211> 450
 <212> DNA
 <213> Cowdria ruminantium

<220>
 <221> CDS
 <222> (1) .. (447)

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 Met His Arg Ser Asn Ile Ile Glu Ile Phe Ile Gly Phe Leu Val Leu
 1 5 10 15

gca gga gca ata tct att ggg ata ata gca ttt aac aaa tta cca tat 96
 Ala Gly Ala Ile Ser Ile Gly Ile Ile Ala Phe Asn Lys Leu Pro Tyr
 20 25 30

aaa aat acc ttg cgt aat tgt tat aca gtt aaa gca ttt ttc tca aat 144
 Lys Asn Thr Leu Arg Asn Cys Tyr Thr Val Lys Ala Phe Phe Ser Asn
 35 40 45

gta gat ggg ttg gac ata gga gat gaa gta aca ata tca gga gta aaa 192
 Val Asp Gly Leu Asp Ile Gly Asp Glu Val Thr Ile Ser Gly Val Lys
 50 55 60

ata ggt aca gta act tca ata tca ttg aat gaa agc tat act cct ata 240
 Ile Gly Thr Val Thr Ser Ile Ser Leu Asn Glu Ser Tyr Thr Pro Ile
 65 70 75 80

gta aca atg tgc ata cag aaa aat atc tta cta cct tca gat agt tca 288
 Val Thr Met Cys Ile Gln Lys Asn Ile Leu Leu Pro Ser Asp Ser Ser
 85 90 95

gca tct ata tta aac agc aat atg tta gga aaa aag cac att gat atc 336
 Ala Ser Ile Leu Asn Ser Asn Met Leu Gly Lys Lys His Ile Asp Ile
 100 105 110

gaa ctt gga tca gat caa gaa gtc atc gta agt gaa ggt tta ata gaa 384
 Glu Leu Gly Ser Asp Gln Glu Val Ile Val Ser Glu Gly Leu Ile Glu

115 120 125
 cat aca cat tca gat tta agt ttc aat gca att att gct aaa ata ata 432
 His Thr His Ser Asp Leu Ser Phe Asn Ala Ile Ile Ala Lys Ile Ile
 130 135 140

 gat tca ctt att aag tag 450
 Asp Ser Leu Ile Lys
 145

<210> 34
 <211> 149
 <212> PRT
 <213> Cowdria ruminantium

<400> 34
 Met His Arg Ser Asn Ile Ile Glu Ile Phe Ile Gly Phe Leu Val Leu
 1 5 10 15

 Ala Gly Ala Ile Ser Ile Gly Ile Ile Ala Phe Asn Lys Leu Pro Tyr
 20 25 30

 Lys Asn Thr Leu Arg Asn Cys Tyr Thr Val Lys Ala Phe Phe Ser Asn
 35 40 45

 Val Asp Gly Leu Asp Ile Gly Asp Glu Val Thr Ile Ser Gly Val Lys
 50 55 60

 Ile Gly Thr Val Thr Ser Ile Ser Leu Asn Glu Ser Tyr Thr Pro Ile
 65 70 75 80

 Val Thr Met Cys Ile Gln Lys Asn Ile Leu Leu Pro Ser Asp Ser Ser
 85 90 95

 Ala Ser Ile Leu Asn Ser Asn Met Leu Gly Lys Lys His Ile Asp Ile
 100 105 110

 Glu Leu Gly Ser Asp Gln Glu Val Ile Val Ser Glu Gly Leu Ile Glu
 115 120 125

 His Thr His Ser Asp Leu Ser Phe Asn Ala Ile Ile Ala Lys Ile Ile
 130 135 140

 Asp Ser Leu Ile Lys
 145